```
1   TTACCAGAACAGCATAACAAGGGCAGGTCTGACTGCAAGCTGGGACTGGGAGGCAGAGCC   60

61  GCCGCCAAGGGGGCCTCGGTTAAACACTGGTCGTTCAATCACCTGCAAGACGAAGAGGCA  120

121 AGGATGCTGTTGGCCTGGGTACAAGCATTCCTCGTCAGCAACATGCTCCTAGCAGAAGCC  180
1     M  L  L  A  W  V  Q  A  F  L  V  S  N  M  L  L  A  E  A     19

181 TATGGATCTGGAGGCTGTTTCTGGGACAACGGCCACCTGTACCGGGAGGACCAGACCTCC  240
20    Y  G  S  G  G  C  F  W  D  N  G  H  L  Y  R  E  D  Q  T  S     39

241 CCCGCGCCGGGCCTCCGCTGCCTCAACTGGCTGGACGCGCAGAGCGGGCTGGCCTCGGCC  300
40    P  A  P  G  L  R  C  L  N  W  L  D  A  Q  S  G  L  A  S  A     59

301 CCCGTGTCGGGGGCCGGCAATCACAGTTACTGCCGAAACCCGGACGAGGACCCGCGCGGG  360
60    P  V  S  G  A  G  N  H  S  Y  C  R  N  P  D  E  D  P  R  G     79

361 CCCTGGTGCTACGTCAGTGGCGAGGCCGGCGTCCCTGAGAAACGGCCTTGCGAGGACCTG  420
80    P  W  C  Y  V  S  G  E  A  G  V  P  E  K  R  P  C  E  D  L     99

421 CGCTGTCCAGAGACCACCTCCCAGGCCCTGCCAGCCTTCACGACAGAAATCCAGGAAGCG  480
100   R  C  P  E  T  T  S  Q  A  L  P  A  F  T  T  E  I  Q  E  A    119

481 TCTGAAGGGCCAGGTGCAGATGAGGTGCAGGTGTTCGCTCCTGCCAACGCCCTGCCCGCT  540
120   S  E  G  P  G  A  D  E  V  Q  V  F  A  P  A  N  A  L  P  A    139

541 CGGAGTGAGGCGGCAGCTGTGCAGCCAGTGATTGGGATCAGCCAGCGGGTGCGGATGAAC  600
140   R  S  E  A  A  A  V  Q  P  V  I  G  I  S  Q  R  V  R  M  N    159

601 TCCAAGGAGAAAAAGGACCTGGGAACTCTGGGCTACGTGCTGGGCATTACCATGATGGTG  660
160   S  K  E  K  K  D  L  G  T  L  G  Y  V  L  G  I  T  M  M  V    179

661 ATCATCATTGCCATCGGAGCTGGCATCATCTTGGGCTACTCCTACAAGAGGGGGAAGGAT  720
180   I  I  I  A  I  G  A  G  I  I  L  G  Y  S  Y  K  R  G  K  D    199
```

FIG.1A

721 TTGAAAGAACAGCATGATCAGAAAGTATGTGAGAGGGAGATGCAGCGAATCACTCTGCCC 780
200 L K E Q H D Q K V C E R E M Q R I T L P 219

781 TTGTCTGCCTTCACCAACCCCACCTGTGAGATTGTGGATGAGAAGACTGTCGTGGTCCAC 840
220 L S A F T N P T C E I V D E K T V V V H 239

841 ACCAGCCAGACTCCAGTTGACCCTCAGGAGGGCAGCACCCCCCTTATGGGCCAGGCCGGG 900
240 T S Q T P V D P Q E G S T P L M G Q A G 259

901 ACTCCTGGGGCCTGAGCCCCCCCAGTGGGCAGGAGCCCATGCAGACACTGGTGCAGGACA 960
260 T P G A * 263

961 GCCCACCCTCCTACAGCTAGGAGGAACTACCACTTTGTGTTCTGGTTAAAACCCTACCAC 1020

1021 TCCCCCGCTTTTTTGGCGAATCCTAGTAAGAGTGACAGAAGCAGGTGGCCCTGTGGGCTG 1080

1081 AGGGTAAGGCTGGGTAGGGTCCTAACAGTGCTCCTTGTCCATCCCTTGGAGCAGATTTTG 1140

1141 TCTGTGGATGGAGACAGTGGCAGCTCCCACAGTGATGCTGCTGCTAAGGGCTTCCAAACA 1200

1201 TTGCCTGCACCCCTGGAACTGAACCAGGGATAGACGGGGAGCTCCCCCAGGCTCCTCTGT 1260

1261 GCTTTACTAAGATGGCTCAGTCTCCACTGTGGGCTTGAGTGGCATACACTGTTATTCATG 1320

1321 GTTAAGGTAAAGCAGGTCAAGGGATGGCATTGAAAAAATATATTTAGTTTTTAAAATATT 1380

1381 TGGGATGGAACTCCCTACTGACCTCTGACAACTGGAAACGAGTTTGTACTGAAGTCAGAA 1440

1441 CTTTGGGTTGGGAATGAGATCTAGGTTGTGGCTGCTGGTATGCTTCAGCTTGCTGGCAAT 1500

1501 GATGTGCCTTGACAACCGTGGGCCAGGCCTGGGCCCAGGGACTCTTCCTGTTTCATAAGG 1560

FIG.1B

1561 AAAGGAAGAATTGCACTGAGCATTCCACTTAGGAAGAGGATAGAGAAGGATCTGCTCCGC 1620

1621 CTTTGGCCACAGGAGCAGAGGCAGACCTGGGATGCCCCAGTTTCTCTTCAGGGATGGATA 1680

1681 GTGACCTGTCTTCATTTTGCACAGGTAAGAGAGTAGTTAGCTAACCTATGGGAATTATAC 1740

1741 TGTGGGGCCTTGTGAGCTGCTTCTAAGAGGCTAACCTGGAAACTAAGCTCAGAGGCAAGG 1800

1801 TAATAAAGCACTTCAGGGCTTGCTCCCCAAGTGGGCCTGATTTAGCAGGTGGTCTGCGGG 1860

1861 CGTCCAGGTCAGCACCTTCCTGTAGGGCACTGGGGCTAGGGTCACAGCCCCTAACTCATA 1920

1921 AAGCAATCAAAGAACCATTAGAAAGGGCTCATTAAGCCTTTTGGACACAGGACCCCAGAG 1980

1981 AGGAAAAAAGTGACTTGCCCAAGGTCGTAAGCAAGCTACTGGCATGGCAAGAGCCCAGCTT 2040

2041 CCTGACGGAGCGCAACATTTCTCCACTGCACTGTGCTAGCAGCTCAGCAGGGCCTCTAAC 2100

2101 CTGTGATGTCACACTCAAGAGGCCTTGGCAGCTCCTAGCCATAGAGCTTCCTTTCCAGAA 2160

2161 CCCTTCCACTGCCCAATGTGGAGACAGGGGTTAGTGGGGCTTTCTATGGAGCCATCTGCT 2220

2221 TTGGGGACCTAGACCTCAGGTGGTCTCTTGGTGTTAGTGATGCTGGAGAAGAGAATATTA 2280

2281 CTGGTTTCTACTTTTCTATAAAGGCATTTCTCTATAAAAAAAAAAAAAA 2329

FIG.1C

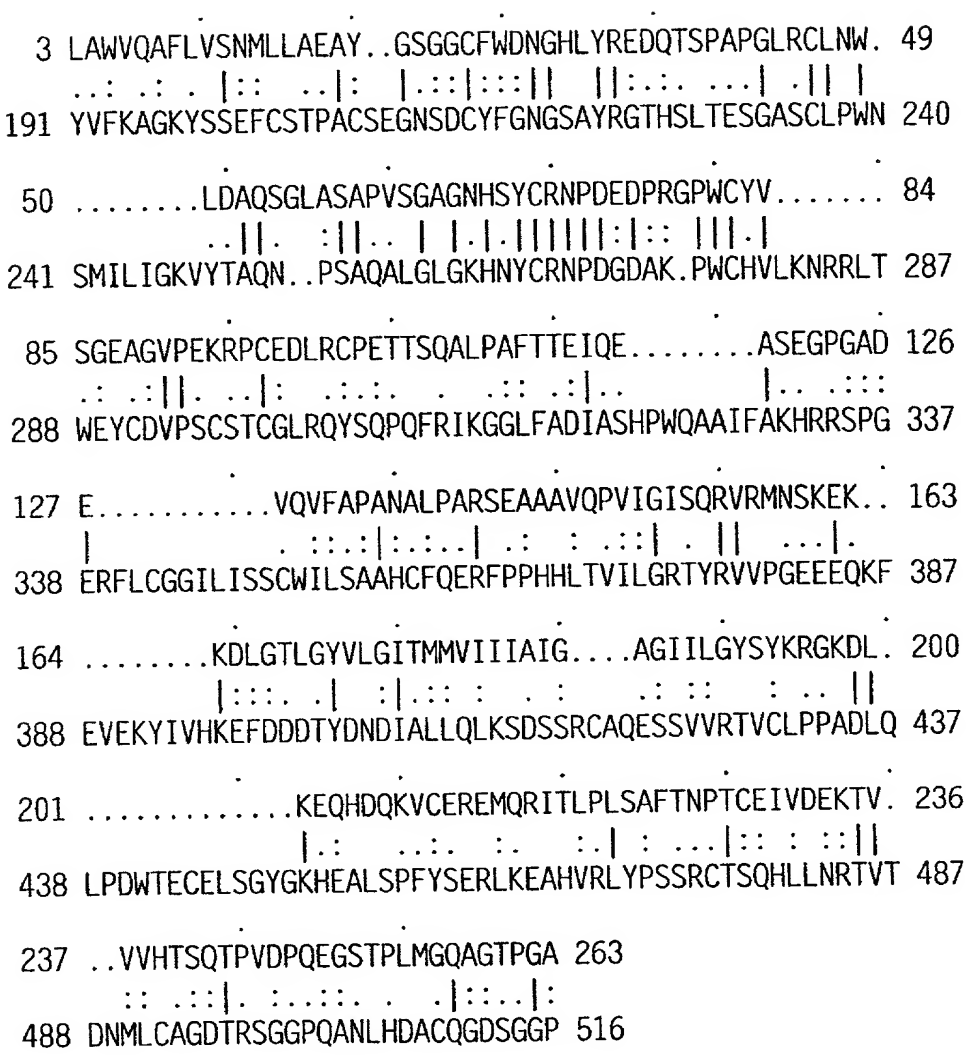
3 LAWVQAFLVSNMLLAEAY..GSGGCFWDNGHLYREDQTSPAPGLRCLNW. 49
191 YVFKAGKYSSEFCSTPACSEGNSDCYFGNGSAYRGTHSLTESGASCLPWN 240
50 .....LDAQSGLASAPVSGAGNHSYCRNPDEDPRGPWCYV..... 84
241 SMILIGKVYTAQN..PSAQALGLGKHNYCRNPDGDAK.PWCHVLKNRRLT 287
85 SGEAGVPEKRPCEDLRCPETTSQALPAFTTEIQE.....ASEGPGAD 126
288 WEYCDVPSCSTCGLRQYSQPQFRIKGGLFADIASHPWQAAIFAKHRRSPG 337
127 E.....VQVFAPANALPARSEAAAVQPVIGISQRVRMNSKEK.. 163
338 ERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVPGEEEQKF 387
164 .....KDLGTLGYVLGITMMVIIIAIG....AGIILGYSYKRGKDL. 200
388 EVEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQ 437
201 .....KEQHDQKVCEREMQRITLPLSAFTNPTCEIVDEKTV. 236
438 LPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVT 487
237 ..VVHTSQTPVDPQEGSTPLMGQAGTPGA 263
488 DNMLCAGDTRSGGPQANLHDACQGDSGGP 516

FIG.2

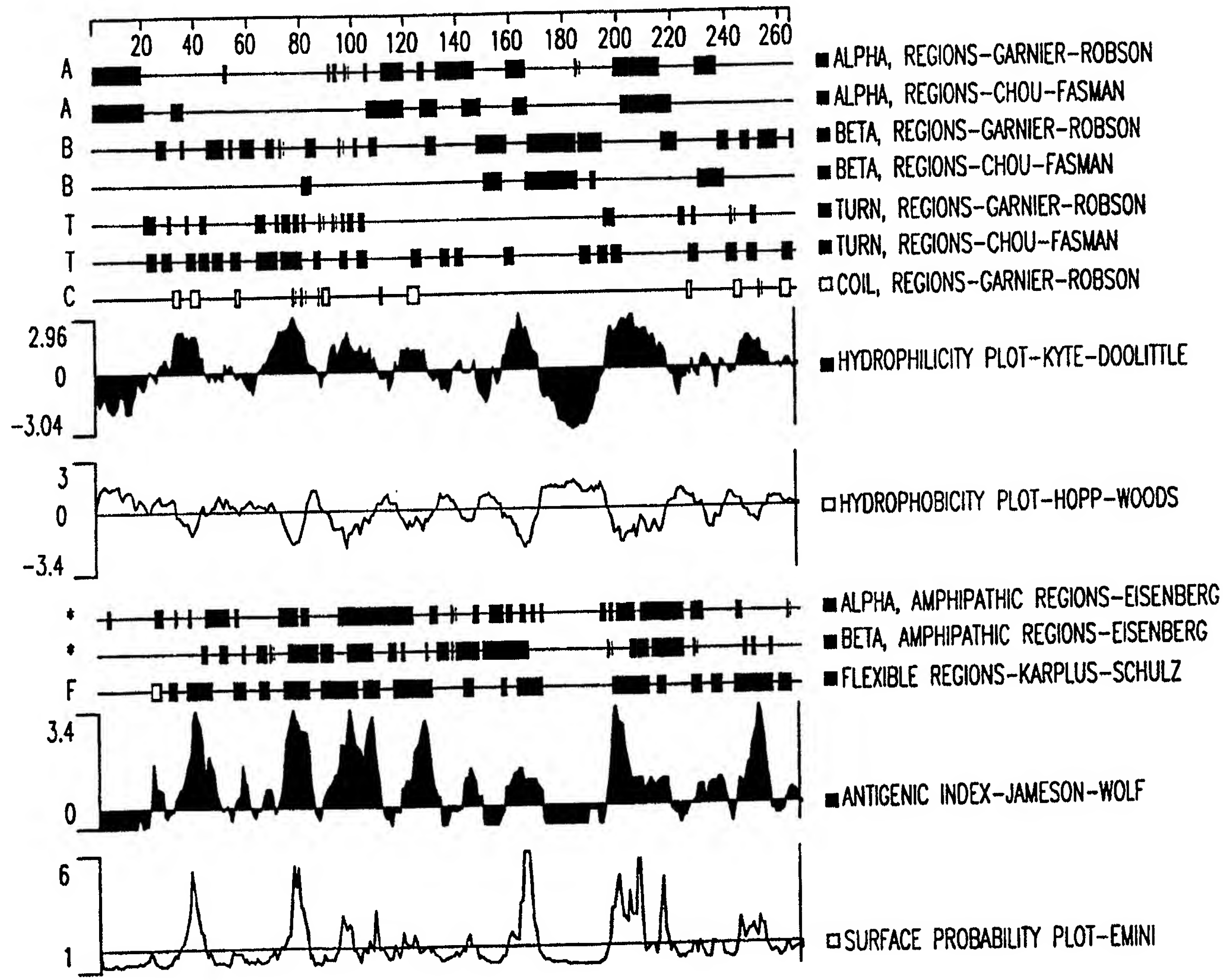
20
40
60
80
100
120
140
160
180
200
220
240
260
A
A
B
B
T
T
C
ALPHA, REGIONS-GARNIER-ROBSON
ALPHA, REGIONS-CHOU-FASMAN
BETA, REGIONS-GARNIER-ROBSON
BETA, REGIONS-CHOU-FASMAN
TURN, REGIONS-GARNIER-ROBSON
TURN, REGIONS-CHOU-FASMAN
COIL, REGIONS-GARNIER-ROBSON
2.96
0
-3.04
HYDROPHILICITY PLOT-KYTE-DOOLITTLE
3
0
-3.4
HYDROPHOBICITY PLOT-HOPP-WOODS
*
*
F
ALPHA, AMPHIPATHIC REGIONS-EISENBERG
BETA, AMPHIPATHIC REGIONS-EISENBERG
FLEXIBLE REGIONS-KARPLUS-SCHULZ
3.4
0
ANTIGENIC INDEX-JAMESON-WOLF
6
1
SURFACE PROBABILITY PLOT-EMINI

FIG.3

TUMOR GROWTH OF t-PALP PROTEIN TRANSFECTANTS ON CAM

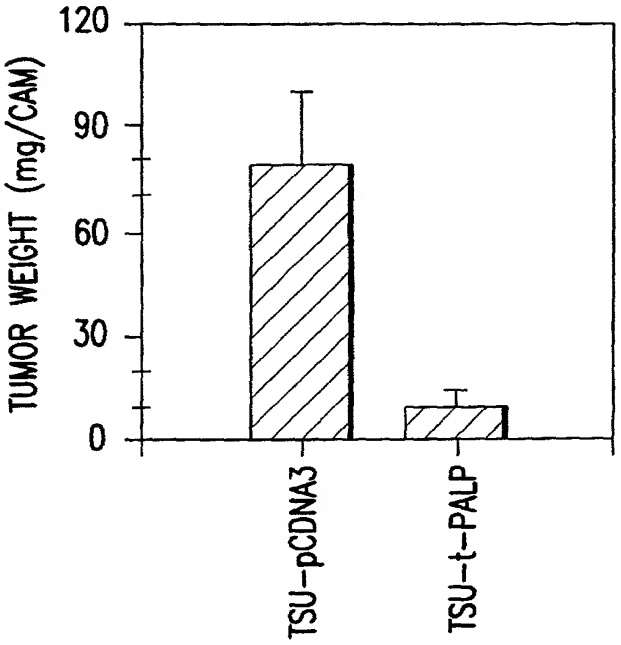

FIG.4

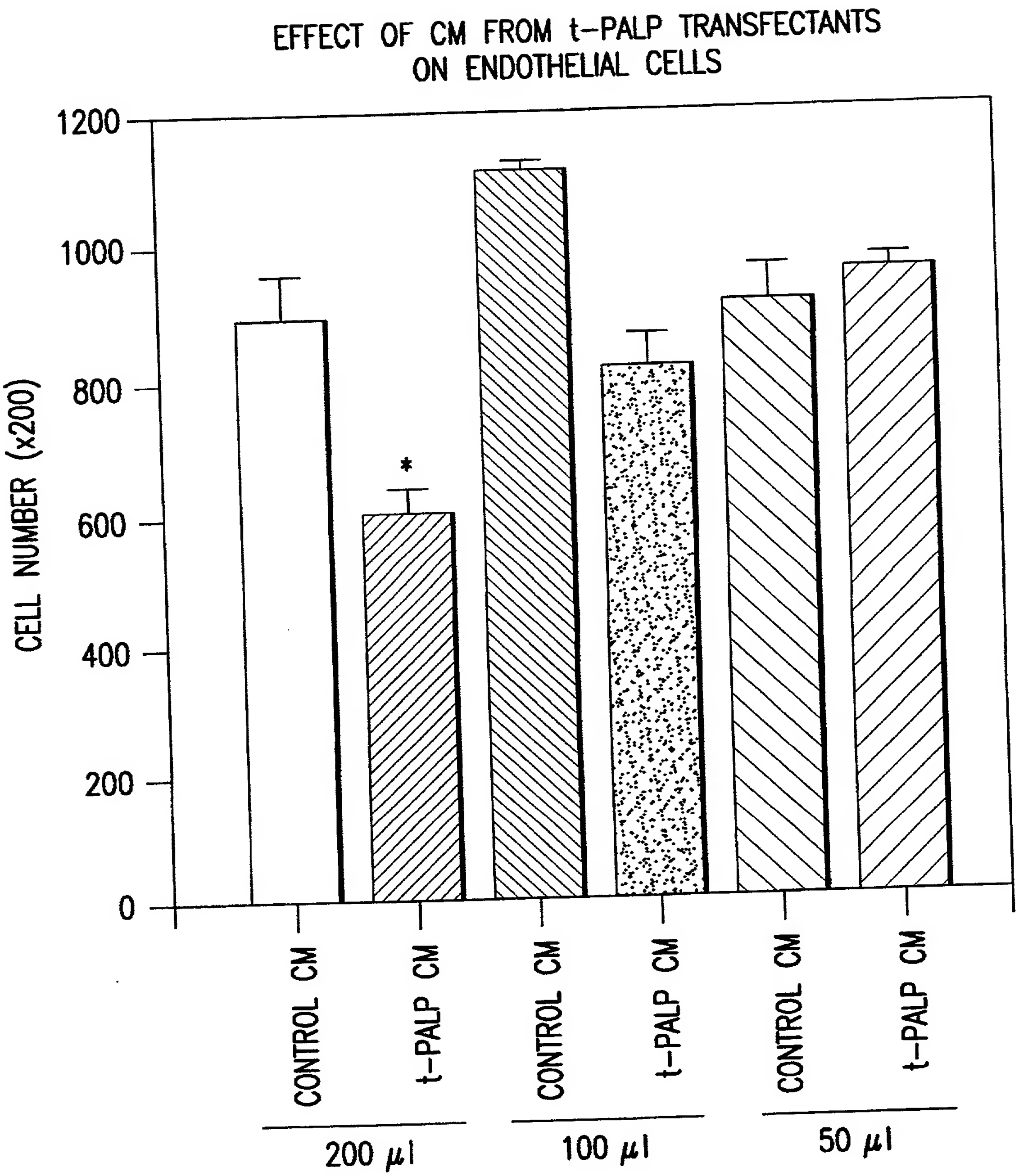

FIG.5

TUMOR GROWTH CURVE OF TSU CELLS TRANSFECTED WITH cDNA OF THE t-PALP PROTEIN

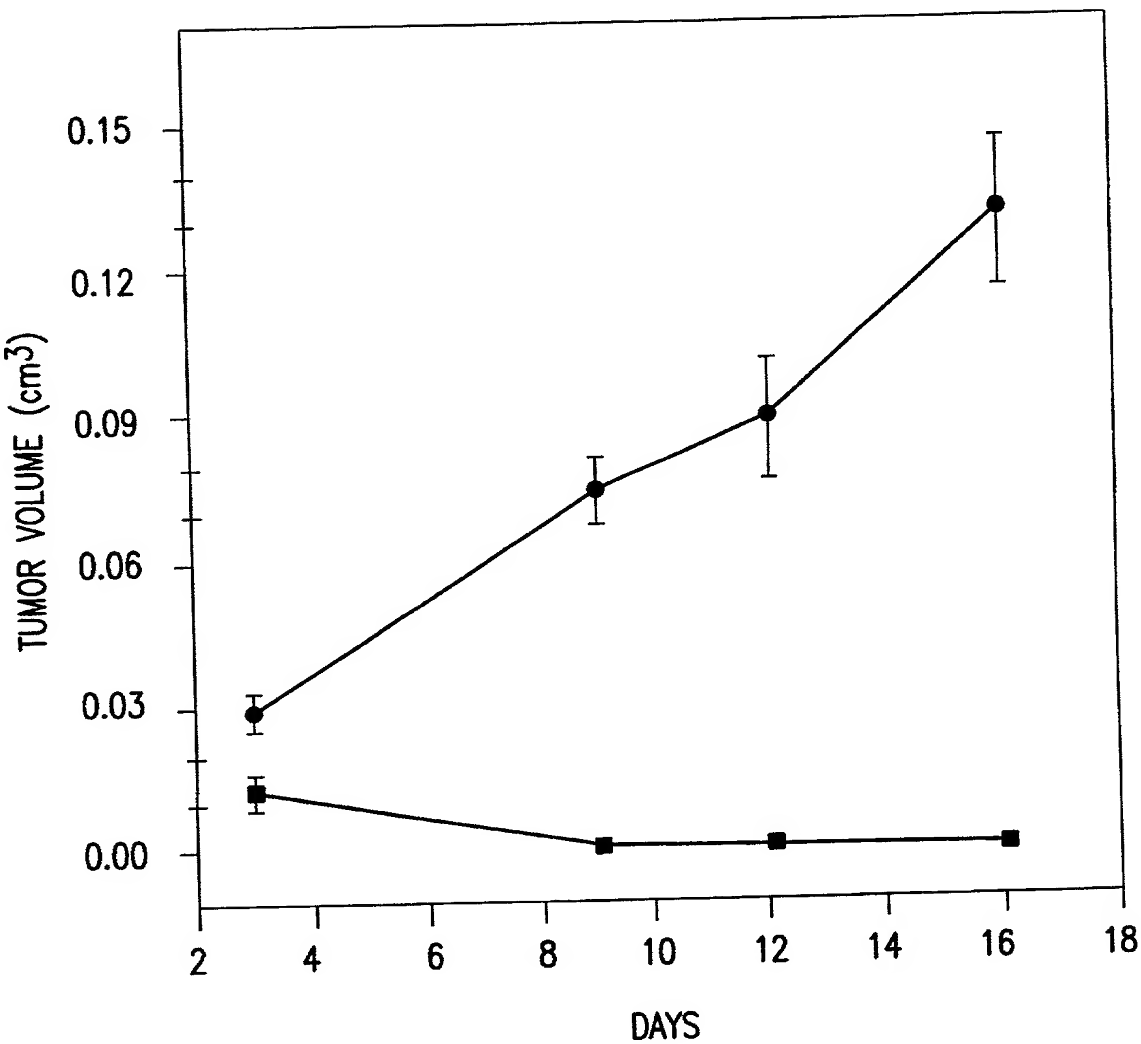

FIG.6